

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1.1	POLO_DROME	576	1	P53304 drosophila		P53304 homo sapien
2	1.0	KPKS_HUMAN	298	1	P07557 homo sapien		P07557 homo sapien
3	1.0	KRAF_MSV36	323	1	P00532 murine sarcoma		P00532 murine sarcoma
4	1.0	KRAB_MOUSE	328	1	P28028 mus musculus		P28028 mus musculus
5	1.0	RMLL_AVIL	367	1	P10533 avian retrovirus		P10533 avian retrovirus
6	1.0	KMIL_AVIMH	380	1	P04531 avian retrovirus		P04531 avian retrovirus
7	1.0	KRAA_MOUSE	437	1	P04527 mus musculus		P04527 mus musculus
8	1.0	RMLL_AVEYL	450	1	P27966 avian retrovirus		P27966 avian retrovirus
9	1.0	YMX1_CAEEL	547	1	P34509 caenorhabditis elegans		P34509 caenorhabditis elegans
10	1.0	PLKL_HUMAN	603	1	P53350 homo sapien		P53350 homo sapien
11	1.0	RMLL_MOUSE	603	1	Q07832 mus musculus		Q07832 mus musculus
12	1.0	PLKL_RAT	603	1	Q62673 rattus norvegicus		Q62673 rattus norvegicus
13	1.0	KRAA_RAT	604	1	P14056 rattus norvegicus		P14056 rattus norvegicus
14	1.0	KRAA_MOUSE	606	1	P10398 homo sapien		P10398 homo sapien
15	1.0	KRAA_PIG	606	1	Q19004 sus scrofa		Q19004 sus scrofa
16	1.0	KRAF_XENIA	638	1	P09560 xenopus laevis		P09560 xenopus laevis
17	1.0	KMIL_CHICK	647	1	P05625 gallus gallus		P05625 gallus gallus
18	1.0	KRAE_HUMAN	648	1	P04049 homo sapien		P04049 homo sapien
19	1.0	KRAF_RAT	765	1	P11345 rattus norvegicus		P11345 rattus norvegicus
20	1.0	KRAF_HUMAN	765	1	P15056 homo sapien		P15056 homo sapien
21	1.0	RMLL_CHICK	806	1	P11346 drosophila melanogaster		P11346 drosophila melanogaster
22	1.0	RMLL_COQJA	807	1	P04982 gallus gallus		P04982 gallus gallus
23	1.0	KRAF_CAEEL	813	1	P34908 coturnix coqui		P34908 coturnix coqui
24	1.0	NPM_CHICK	294	1	Q07992 caenorhabditis elegans		Q07992 caenorhabditis elegans
25	9	KRAS_AVISU	402	1	KRAS_AVISU		KRAS_AVISU
26	9	KRAS_CHICK	507	1	KRAS_CHICK		KRAS_CHICK
27	9	KP68_MOUSE	515	1	KP68_MOUSE		KP68_MOUSE
28	9	KRAS_CHICK	607	1	YJK0_MOUSE		YJK0_MOUSE
29	9	HRL_MOUSE	619	1	P43951 saccharomyces cerevisiae		P43951 saccharomyces cerevisiae
30	9	HRL_RABBIT	620	1	O94299 mus musculus		O94299 mus musculus
31	9	HRL_RAT	626	1	P51915 rattus norvegicus		P51915 rattus norvegicus
32	9	HRL_RABBIT	683	1	P33279 oryctolagus cuniculus		P33279 oryctolagus cuniculus
33	9	PLOI_SCHPO	0.5		P50528 schizosaccharomyces pombe		P50528 schizosaccharomyces pombe

ALIGMENTS							
Scoring table: OLIGO Gapop 60.0 , Gapext. 60.0							
Searched: 93435 seqs, 34255486 residues							
Word size : 0							
Total number of hits satisfying chosen parameters: 93435							
Minimum DB seq length: 0							
Maximum DB seq length: 2000000000							
Post-processing: Listing first 45 summaries							
Database : SwissProt_39;*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
RESULT 1	POLO_DROME	STANDARD;	PRT;	576 AA.			
ID P5304;	POLO_DROME						
AC P25977	rattus norvegicus						
CC7_SCHPO	schizosaccharomyces pombe						
TYK2_HUMAN	homo sapiens						
GCN2_YEAST	saccharomyces cerevisiae						
KROS_HUMAN	homo sapiens						
PROTEIN KINASE POLO (EC 2.7.1. -)	homo sapiens						
POLO	drosophila melanogaster						
DROSOPHILA	drosophila melanogaster						
EUKARYOTA	eukaryotes						
Metazoa	metazoans						
Insecta	insects						
Pterygota	pterygotes						
Endopterygota	endopterygotes						
Brachycera	brachycerans						
Muscomorpha	muscomorphans						
[1]							
RN TAxID-7227;							
RP SEQUENCE FROM N.A.							
RC STRAIN=CANTON-S;							
RX MEDLINE=92084000; PubMed=16608828;							
RA Llamazares S., Moreira A., Girdham C., Spruce B.A., Gonzalez C., Marek R.E., Glover D.M., Sunkel C.E.; Polo encodes a protein kinase required for mitosis in Drosophila.							
RT Genes Dev. 5:2153-2165(1991).							
CC FUNCTION: MAY PLAY A ROLE IN REGULATING BOTH NUCLEAR AND CYTOPLASMIC ASPECTS OF THE MITOTIC CYCLE.							
CC SUBCELLULAR LOCATION: CYTOPLASMIC.							
CC TISSUE SPECIFICITY: LARVAL DISCS, BRAIN AND TESTIS.							
CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES, CDC5/POLO SUBFAMILY.							
CC							
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CC							
DR EMBL; X63361; CA44963.1; -							
DR FLYBASE; FBgn003124; FlyBase.							
DR InterPro; IPR000719; -							
DR InterPro; IPR00959; -							
DR InterPro; IPR00290; -							
DR PFAM; PF00059; POLO_box..2.							
DR PFAM; PF00069; Pkinase..1.							
DR PROSITE; PS00101; PROTEIN_KINASE_ATP; FALSE_NEG.							
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.							
KW Transferase; Serine/threonine-protein kinase; ATP-binding DOMAIN 25 277 PROTEIN KINASE.							
FT NP_BIND BINDING 31 39 ATP (BY SIMILARITY).							
FT ACT_SITE 148 54 BY SIMILARITY.							
FT DOMAIN 394 420 POLO-HOMOLOGY (PH2).							
SQ SEQUENCE 576 AA; 66947 MW; B957BDA173FA57D3 CRC64;							

Query Match 0.7%; Score 11; DB 1; Length 576;
 Best Local Similarity 100.0%; Pred. No. 0.017; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 861 HVKIGDFGLAT 871
 Db 161 HVKIGDFGLAT 171

RESULT 2
 KPKS_HUMAN STANDARD:
 ID KPKS_HUMAN PRT; 298 AA.
 AC P07557;
 DT 01-APR-1988 (Rel. 07, Created)
 RX 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE PKS PROTO-ONCOGENE SERINE/TREONINE-PROTEIN KINASE (EC 2.7.1.-.)
 DE ARAF2 OR PKS OR PKS1. (FRAGMENT).
 OS Homo sapiens (Human).
 OC Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84121298; PubMed=6320371;
 RA Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
 RA "A common onc gene sequence transduced by avian carcinoma virus MH2
 and by murine sarcoma virus 3611.";
 RT Science 223:813-816(1984);
 RL RN
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84172180; PubMed=6324342;
 RA Mark G.E., Rapp U.R.;
 RA "Primary structure of v-raf: relatedness to the src family of
 oncogenes."
 RT Science 224:285-289(1984).
 CC POLYPROTEIN.
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-RAF
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -!- MIL/RAF SUBFAMILY.
 CC
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 CC
 DR EMBL: M13829; AAB0754.1; -.
 DR PIR: A23341; TVHUPK.
 DR HSSP: P00523; 2PTK.
 DR InterPro: IPR00719; -.
 DR InterPro: IPR002290; -.
 DR Pfam: PF00069; kinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50012; Serine/threonine-protein kinase; proto-oncogene;
 KW ATP-binding.
 FT NON_TER 1 1 PROTEIN KINASE.
 FT DOMAIN 19 279 ATP (BY SIMILARITY).
 FT NP_BIND 25 33 ATP (BY SIMILARITY).
 FT BINDING 45 45 BY SIMILARITY.
 FT ACT_SITE 138 138 BY SIMILARITY.
 SQ SEQUENCE 298 AA; 33852 MW; 9RC38F66A7AAFFDD0 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 298;
 Best Local Similarity 100.0%; Pred. No. 0.099; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871
 Db 152 VKIGDFGLAT 161

RESULT 3
 KRAF_MSV36 STANDARD:
 ID KRAF_MSV36 STANDARD;
 AC P00332;

Query Match 0.6%; Score 10; DB 1; Length 323;
 Best Local Similarity 100.0%; Pred. No. 0.11; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 862 VKIGDFGLAT 871
 Db 157 VKIGDFGLAT 166

RESULT 4
 KRAB_MOUSE STANDARD:
 ID KRAB_MOUSE STANDARD;
 AC P28028;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE B-RAF PROTO-ONCOGENE SERINE/TREONINE-PROTEIN KINASE (EC 2.7.1.-.)
 DE (FRAGMENT).
 GN BRAF OR B-RAF.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus .
 OX NCBI_TAXID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91271351; PubMed=2052597;
 RA Reynolds S.H.; Crescenzi M.; Molloy C.J.; Blam S.B.,
 RA "Development of a highly efficient expression cDNA cloning system:
 RT application to oncogene isolation";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5167-5171 (1991).
 CC -!- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS
 CC FROM THE CELL MEMBRANE TO THE NUCLEUS.
 CC -!- FUNCTION: MAY PLAY A ROLE IN THE POSTSYNAPTIC RESPONSES OF
 CC HIPPOCAMPAL NEURON.
 CC -!- DISEASE: PARTICIPATES IN A CHROMOSOMAL TRANSLOCATION THAT PRODUCES
 CC A TIFLIA-BRAF (T18) ONCOGENE ORIGINALLY ISOLATED FROM A FURFURAL-
 CC INDUCED HEPATOMA.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.

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 CC or send an email to license@isb-sib.ch).
 DR EMBL: M64429; AAA37320.1; ALT_INIT.
 DR PIR: A4951; TWSBF.
 DR HSSP: P11362; IFGI.
 DR MGDB: MGI:381190; Braf.
 DR InterPro: IPR00719; .
 DR InterPro: IPR002490; .
 DR Pfam: PF00069; Pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; Proto-oncogene;
 KW ATP-Linding; Chromosomal translocation.
 FT DOMAIN 1 1
 FT DOMAIN 19 279 PROTEIN KINASE.
 FT NP_BIND 25 33 ATP (BY SIMILARITY).
 FT BINDING 45 45 ATP (BY SIMILARITY).
 FT ACT_SITE 138 138 BY SIMILARITY.
 SQ SEQUENCE 328 AA: 36986 MW: 67A2BFB78A78E3D CRC64;

Query Match 0.6%; Score 10; DB 1; Length 328;

Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Score 10; DB 1; Length 367;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

ID RMIL_AVIMH STANDARD; PRT; 367 AA.
 AC P10533; Q85612; Q85613; Q85614;
 DT 01-JUL-1989 (Rel. 1.1, Created)
 DT 01-JUL-1989 (Rel. 1.1, Last sequence update)
 DT 01-OCT-2000 (Rel. 4.0, Last annotation update)
 DE RMIL SERINE/THREONINE-PROTEIN KINASE TRANSFORMING PROTEIN
 DE (EC 2.7.1.-).
 GN V-RMIL.
 OC Avian retrovirus IC10.
 OX Viruses; Retroviridae; Avian type C retroviruses.

OC V-RMIL viruses; Retroviral viruses; Retroviridae; Avian type C retroviruses.

OX NCBI_TAXID=11874;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84191511; PubMed=6325930;
 RA Sutrave P., Bonner T.I., Rapp U.R., Jansen H.W., Patschinsky T.,

RX MEDLINE=89160254; PubMed=2537952;
 RA Eychene A., Marx M., Dezelée P., Calothy G.;
 RT "Complete nucleotide sequence of IC10, a retrovirus containing the
 RT feline oncogene transduced in chicken neuroretina cells infected with
 RT avian retrovirus RAV-1.";
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89091077; PubMed=285163;
 RA Marx M., Eychene A., Laugier D., Bechade C., Crisanti P.,
 RA Dezelée P., Pessac B., Calothy G.;
 RT "A novel oncogene related to c-mil is transduced in chicken
 RT neuroretina cells induced to proliferate by infection with an avian
 RT lymphomatosis virus.";
 RL EMBO J. 7:3369-3373 (1988).
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-R-MIL
 CC POLYPROTEIN.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MIL/RAF SUBFAMILY.

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 CC --

DR EMBL: X13744; CAA32008.1; ALT_SEQ.
 DR EMBL: X12438; CAA31790.1; ALT_SEQ.
 DR PIR: S01645; TVFVM.
 DR HSSP: P11362; IFGI.
 DR InterPro: IPRO00719; .
 DR InterPro: IPRO02230; .
 DR PIR; S01645; TVFVM.
 DR Pfam: PF00069; Pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Polypeptide; Transforming protein; Serine/threonine-protein kinase;
 KW Transferase; Oncogene; ATP-binding.
 FT DOMAIN 67 327 PROTEIN KINASE.
 FT NP_BIND 73 81 ATP (BY SIMILARITY).
 FT BINDING 93 93 ATP (BY SIMILARITY).
 FT ACT_SITE 186 186 BY SIMILARITY.
 SQ SEQUENCE 367 AA: 41023 MW: E1374FCDCB9398A CRC64;

Query Match 0.6%; Score 10; DB 1; Length 367;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6

ID RMIL_AVIMH STANDARD; PRT; 380 AA.
 AC P00531.
 DT 21-JUL-1986 (Rel. 0.1, Created)
 DT 21-JUL-1986 (Rel. 0.1, Last sequence update)
 DT 01-OCT-2000 (Rel. 4.0, Last annotation update)
 DE M1L SERINE/THREONINE-PROTEIN KINASE TRANSFORMING PROTEIN
 DE (EC 2.7.1.-).
 GN V-MIL OR V-MHT.
 OS Avian retrovirus MH2.
 OC Viruses; Retroviral viruses; Retroviridae;
 OX NCBITaxID=11870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84191511; PubMed=6325930;
 RA Sutrave P., Bonner T.I., Rapp U.R., Jansen H.W., Patschinsky T.,

RA Bister K.;
 RT "Nucleotide sequence of avian retroviral oncogene v-mil: homologue of v-raf oncogene";
 RT murine retroviral oncogene v-raf.";
 RL Nature 309:85-88(1984).
 [2]
 RN
 RP SEQUENCE FROM N.A. MEDLINE=84121298; PubMed=6320371;
 RA Kan N.C., Flordelis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
 RT "A common onc gene sequence transduced by avian carcinoma virus MH2 and by murine sarcoma virus 3611.";
 RL Science 223:813-816(1984).
 CC -1- DISEASE: BY ITSELF THE V-MIL ONCOGENE HAS ONLY WEAK TRANSFORMING CAPACITY BUT IT ABOLISHES THE GROWTH FACTOR REQUIREMENTS OF AVIAN MACROPHAGES TRANSFORMED BY OTHER ONCOGENES.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-MHT OR GAG-MIL POLYPEPTIDE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1- MIL/RAF SUBFAMILY.

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DR EMBL: D00024; BA00018.1;
 DR EMBL: M13071; AAA37258.1;
 DR PIR: A55382; TVNSRF.
 DR HSSP: P11362; IFGI.
 DR MGD: MGI:88065; Araf.
 DR Interpro; IPR00719; -.
 DR Interpro; IPR002390; -.
 DR Pfam; PF00069; pkinase_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS05011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; ATP-binding.
 DR KW ATP-binding.
 DR HSSP: P11362; IFGI.
 DR Interpro; IPR00719; -.
 DR Interpro; IPR002390; -.
 DR Pfam; PF00069; pkinase_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE; PS05011; PROTEIN_KINASE_DOM; 1.
 KW Polypeptide; Transforming protein; Serine/threonine-protein kinase; KW Transerase; Oncogene; ATP-binding.
 KW DOMAIN 82 PROTEIN_KINASE.
 FT 341 ATP (BY SIMILARITY).
 FT DOMAIN 88 96 Pred. No. 0.14;
 FT NP_BIND 108 108 ATP (BY SIMILARITY).
 FT BINDING 201 201 BY SIMILARITY.
 FT ACT_SITE 211 211 G > E (IN REF. 2)
 FT CONFLICT 380 AA; 42853 MW: 6498695FB7EBEE5D CRC64;
 SQ

Query Match 0.6%; Score 10; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 ID RMIL_AVEVR STANDARD; PRT; 450 AA.
 AC P27966;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-OCT-2000 (Rel. 23, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE RMIL_SERINE/THREONINE-PROTEIN KINASE TRANSFORMING PROTEIN DE (EC 2.7.1.).
 DE V-RMIL.
 GN Marx M.;
 OS Avian rous-associated virus type 1.
 OC Viruses; Retroviridae; Avian type C retroviruses.
 OC Virus; Retroviridae; Avian type C retroviruses.
 NCBI_TaxID=11930;
 OX RN [1]
 RN SEQUENCE FROM N.A.
 RN MEDLINE=91:5125; PubMed=1645786;
 RX Felder M.P.; Echene A.; Barnier J.V.; Calogeraki I.; Calothy G.;
 RA RT "Common mechanism of retrovirus activation and transduction of c-mil and c-Rmil in chicken neuroretina cells infected with Rous-associated virus type 1."
 RL J. Virol. 65:3633-3640(1991).
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A R-MIL-ENV POLYPROTEIN.
 CC SEQUENCE FROM N.A.
 RN MEDLINE=97064566; PubMed=3491291;
 RX Huleihel M., Goldsborough M., Cleveland J., Gunnell M., Bonner T.,
 NCBI_TaxID=10090;

RA RESULT 7
 ID KRAA_MOUSE STANDARD; PRT; 437 AA.
 AC P04627;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1. -)
 DE (FRAGMENT).
 GN ARAF OR ARAF OR A-RAF.
 OS Mus musculus (Mouse);
 OC Mammalia; Eutheria; Rodentia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX RA

RN SEQUENCE FROM N.A.
 RN MEDLINE=97064566; PubMed=3491291;
 RX Huleihel M., Goldsborough M., Cleveland J., Gunnell M., Bonner T.,

5

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CC EMBL; L15314; AAA38084-1; ~.

CC PIR; S44841; S44841; ~.

CC HSSP; 063450; 1A06; Wormpep; K06H.; 1; CE00252.

CC InterPro; IPR000719; ~.

CC InterPro; IPR002230; ~.

CC PRAM; PF00063; kinase; 1.

CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

CC Hypothetical protein; Transferase; Serine/threonine-protein kinase; ATP-binding domain; 267 526 PROTEIN KINASE.

CC NP_BIND 273 281 ATP (BY SIMILARITY).

CC BINDING 296 296 ATP (BY SIMILARITY).

CC ACT_SITE 390 390 BY SIMILARITY.

CC SEQUENCE 547 AA; 63490 MW; OOD28C2FEAC63101 CRC64;

Query Match 0.68; Score 10; DB 1; Length 547;

Best Local Similarity 100.0%; Pred. No. 0.17;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 862 VKIGDFGLAT 871

Db 404 VKIGDFGLAT 413

RESULT 10

ID	PLK1_HUMAN	STANDARD:	PRT:	603 AA.
AC	P53350;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DE	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	SERINE/THREONINE PROTEIN KINASE PLK (EC 2.7.1.-) (PLK-1) (SERINE-THREONINE PROTEIN KINASE 13) (STPK13).			
GN	PLK OR PLK1.			
OS	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TAXID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Placenta;			
RX	MBIDLINE=94289293; PubMed=8018557;			
RA	Hamanaka R., Malloid S., Smith M.R., O'Connell C.D., Longo D.L., Perris D.K.;			
RA	*Cloning and characterization of human and murine homologues of the Drosophila polo serine-threonine kinase.;			
RL	Cell Growth Differ. 5:249-257(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MBIDLINE=94067140; PubMed=7902533;			
RA	Lake R.J., Jeinek W.R.;			
RA	*Cell cycle- and terminal differentiation-associated regulation of the mouse mRNA encoding a conserved mitotic protein kinase.;			
RL	Mol. Cell. Biol. 13:7793-7801(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MBIDLINE=95051109; PubMed=7962193;			
RA	Golsteyn R.M., Schultz S.J., Bartek J., Ziomecki A., Ried T., Nigg E.A.;			
RA	*Cell cycle analysis and chromosomal localization of human Plk1, a putative homologue of the mitotic kinases Drosophila polo and Saccharomyces cerevisiae Cdc5.;			
RL	J. Cell. Sci. 107:1509-1517(1994).			

DR	PROSITE; PS00107; PROTEIN_KINASE_ST; 1.	KW	Nuclear protein.
DR	PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.	FT	DOMAIN 53
KW	transferase; Serine/threonine-protein kinase; ATP-binding;	FT	NP_BIND 59
KW	nuclear protein.	FT	BINDING 82
CC	PROTEIN_KINASE.	FT	ACT_SITE 176
DOMAIN	305	FT	DOMAIN 176
NP_BIND	59	FT	ATP (BY SIMILARITY).
FT	82	FT	POLG-HOMOLOGY (PH2).
BINDING	82	SQ	SEQUENCE 603 AA; 107AFFB3B7EDC002 CRC64; ;
ACT_SITE	176		
DOMAIN	410		
FT	439		
CONFICT	4		
FT	15		
CONFICT	15		
FT	23		
CONFICT	23		
FT	27		
CONFICT	27		
FT	29		
CONFICT	29		
FT	41		
CONFICT	41		
FT	54		
CONFICT	495		
SEQUENCE	603 AA;		
	1B980646366EFA10 CRC64; ;		
RESULT	13		
	KRAA_RAT		
ID	KRAA_RAT		
			STANDARD; PRT; 604 AA.
AC	P14056;		
			SEQUENCE FROM N.A.
RC	STRAIN=FISCHER; TISSUE=Liver;		
DT	01-JAN-1990 (Rel. 13, Created)		
DT	01-OCT-1990 (Rel. 13, Last sequence update)		
DE	01-OCT-2000 (Rel. 40, Last annotation update)		
GN	A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-).		
RA	Rattus norvegicus (Rat).		
RA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
NCBI_TAXID	10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=FISCHER; TISSUE=Liver;		
MEDLINE	=8821724; Published=344979;		
RX			
RA	Ishikawa F., Takaku F., Nagao M., Sugimura T.;		
RT	"The complete primary structure of the rat A-raf cDNA coding region: A-RAF1 OR A-RAF."		
RT	conservation of the putative regulatory regions present in rat c-raf."		
RL	Oncogene Res. 1: 243-253(1987).		
CC	-I- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS		
CC	FROM THE CELL MEMBRANE TO THE NUCLEUS.		
CC	-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
CC	MIL/RAF SUBFAMILY.		
CC	-I- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAIN.		
CC			
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CC			
CC	SEQUENCE FROM N.A.		
RC	TISSUE=Pancreas;		
RA	Anistrup J., Hansen J.A., Hixlris Nielsen J.		
CC	Submitted (MAY-1994) to the EMBL/GerBank/DDJB databases.		
CC	-I- FUNCTION: MAY BE REQUIRED FOR CELL DIVISION AND MAY HAVE A ROLE DURING G1 OR S PHASE (BY SIMILARITY).		
CC	-I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).		
CC	-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
CC	CDC5/POLO SUBFAMILY.		
CC			
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CC			
DR	EMBL; X06942; CAA30023; 1; -.		
DR	PRINTS; PRO0008; DAGPE DOMAIN.		
DR	HSSP; P04049; 1FAQ.		
DR	PS00726; S00726.		
DR	InterPro; IPR00719; DAG_Pe_bind_DOM_1; 1.		
DR	InterPro; IPR002219; -.		
DR	InterPro; IPR002219; -.		
DR	InterPro; IPR002219; -.		
DR	PF00130; DAG_Pe-bind; 1.		
DR	Pfam; PF00069; Pkinase_1.		
DR	PRINTS; PRO0008; DAGPE DOMAIN.		
DR	PS00479; DAG_Pe_bind_DOM_1; 1.		
DR	PROSITE; PS50081; DAG_Pe_BIND_DOM_2; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
DR	Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;		
KW	ATP-binding; Phorbol-ester binding.		
FT	DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.		
FT	PROTEIN_KINASE.		
KW	Transferase; Serine/threonine-protein kinase; ATP-binding;		

8

FT NP_BIND 314 322 ATP (BY SIMILARITY).	DR PROSITE; PS00479; DAG_PEBIND_DOM_1; 1.
FT BINDING 334 334 (BY SIMILARITY).	DR PROSITE; PS50081; DAG_PEBIND_DOM_2; 1.
FT ACT_SITE 427 427 BY SIMILARITY.	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
FT SEQUENCE 604 AA; FF24FB2170B0B115 CRC64;	DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
FT SEQUENCE 604 AA; PS00108; PROTEIN_KINASE_ST; 1.	DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
	KW Transferase; Serine/threonine-protein kinase; Proto-oncogene; Zinc; ATP-binding; Phorbol-ester binding.
	KW PHORBOL-ESTER AND DAG BINDING.
	FT DOMAIN 99 144 Phorbol-ester binding.
	FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.
	FT DOMAIN 99 144 PROTEIN KINASE.
	FT NP_BIND 310 570 ATP (BY SIMILARITY).
	FT BINDING 316 324 ATP (BY SIMILARITY).
	FT BINDING 336 336 ATP (BY SIMILARITY).
	FT ACT_SITE 429 429 BY SIMILARITY.
	SEQUENCE 606 AA; D23E571130AA468 CRC64;
	Query Match 0.6%; Score 10; DB 1; Length 606;
	Best Local Similarity 100.0%; Pred. No. 0.18; PRT; 606 AA.
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0; Gaps 0;
Qy 862 VKIGDFGLAT 871	Query Match 0.6%; Score 10; DB 1; Length 606;
Db 441 VKIGDFGLAT 450	Best Local Similarity 100.0%; Pred. No. 0.18; PRT; 606 AA.
	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;
	RESULT 15
	KRAA_PIG STANDARD; PRT; 606 AA.
	ID KRAA_PIG STANDARD; PRT; 606 AA.
	AC O1904; VKIGDFGLAT 871
	DT 15-JUL-1998 (Rel. 36, Created)
	DT 15-JUL-1998 (Rel. 36, Last sequence update)
	DT 01-OCT-2000 (Rel. 40, Last annotation update)
	DE A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-)
	(ONCOGENE PKS2).
	GN ARAF.
	OS Homo sapiens (Human).
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
	NCBI_TaxID=9606;
	[1]
	SEQUENCE FROM N.A.
	MEDLINE=87146380; PubMed=3029685;
	Beck T.W., Huleihel M., Gunnell M., Bonner T.I.; Rapp U.R.; PT "The complete coding sequence of the human A-raf-1 oncogene and transforming activity of a human A-raf carrying retrovirus.";
	RT Nucleic Acids Res. 15:595-609(1987).
	[2]
	SEQUENCE FROM N.A.
	MEDLINE=94292185; PubMed=8020955;
	Lee J.E., Beck T.W., Brennsecheidt U., Degennaro L.J., Rapp U.R.; RT "The complete sequence and promoter activity of the human A-raf-1 gene (ARAF1)."; RA Yasue H., Adams L., Ozawa A., Hanazono M., Li N., Lin Z.H., RA Kusumoto H.; RT "Assignment of ARAF1 to porcine chromosome Xp11.2-p13 by fluorescence in situ hybridization.";
	RL Mamm. Genome 8:457-458(1997).
	CC -1- FUNCTION: INVOLVED IN THE TRANSDUCTION OF MITOGENIC SIGNALS FROM THE CELL MEMBRANE TO THE NUCLEUS (BY SIMILARITY).
	CC -1- TISSUE SPECIFICITY: PREDOMINANTLY IN UROGENITAL TISSUES (BY SIMILARITY).
	CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
	CC -1- SIMILARITY: MIL/RAF SUBFAMILY.
	CC -1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAIN.
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	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licensee@isb-sib.ch).
	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licensee@isb-sib.ch).
	CC EMBL; D88285; BAA22379; 1; -.
	DR HSSP; P04049; 1FAQ.
	DR InterPro; IPR002219; -.
	DR InterPro; IPR002290; -.
	DR Pfam; PF00130; DAG_PEBind; 1.
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	DR PROSITE; PS50081; DAG_PEBIND_DOM_2; 1.
	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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	DR InterPro; IPR002219; -.
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	DR InterPro; IPR002219; -.
	DR InterPro; IPR002290; -.
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	DR Pfam; PF00069; pkinase; 1.
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	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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	DR InterPro; IPR002290; -.
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	DR Pfam; PF00069; pkinase; 1.
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	DR PROSITE; PS50081; DAG_PEBIND_DOM_2; 1.
	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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	DR InterPro; IPR002290; -.
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	DR InterPro; IPR002219; -.
	DR InterPro; IPR002290; -.
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	DR PROSITE; PS50081; DAG_PEBIND_DOM_2; 1.
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	DR InterPro; IPR002219; -.
	DR InterPro; IPR002290; -.
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	DR PROSITE; PS50081; DAG_PEBIND_DOM_2; 1.
	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
	DR PROSITE; PS00069; pkinase; 1.
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	Pfam; PF00069; pkinase; 1.
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	DR InterPro; IPR002219; -.
	DR InterPro; IPR002290; -.
	DR Pfam; PF00130; DAG_PEBind; 1.
	DR Pfam; PF00069; pkinase; 1.
	DR PRINTS; PR00068; DAGPDOMAIN.
	DR PROSITE; PS00479; DAG_PEBIND_DOM_1; 1.
	DR PROSITE; PS50081; DAG_PEBIND_DOM_2; 1.
	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
	DR PROSITE; PS00069; pkinase; 1.
	PRINTS; PR00068; DAGPDOMAIN.
	Pfam; PF00069; pkinase; 1.
	PRINTS; PR00068; DAGPDOMAIN.
	DR InterPro; IPR000719; -.
	DR InterPro; IPR002219; -.
	DR InterPro; IPR002290; -.
	DR Pfam; PF00130; DAG_PEBind; 1.
	DR Pfam; PF00069; pkinase; 1.
	DR PRINTS; PR00068; DAGPDOMAIN.
	DR PROSITE; PS00479; DAG_PEBIND_DOM_1; 1.
	DR PROSITE; PS50081; DAG_PEBIND_DOM_2; 1.
	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
	DR PROSITE; PS00069; pkinase; 1.
	PRINTS; PR00068; DAGPDOMAIN.
	Pfam; PF00069; pkinase; 1.
	PRINTS; PR00068; DAGPDOMAIN.
	DR InterPro; IPR000719; -.
	DR InterPro; IPR002219; -.
	DR InterPro; IPR002290; -.
	DR Pfam; PF00130; DAG_PEBind; 1.
	DR Pfam; PF00069; pkinase; 1.
	DR PRINTS; PR00068; DAGPDOMAIN.
	DR PROSITE; PS00479; DAG_PEBIND_DOM_1; 1.
	DR PROSITE; PS50081; DAG_PEBIND_DOM_2; 1.
	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
	DR PROSITE; PS00069; pkinase; 1.
	PRINTS; PR00068; DAGPDOMAIN.
	Pfam; PF00069; pkinase; 1.
	PRINTS; PR00068; DAGPDOMAIN.
	DR InterPro; IPR000719; -.
	DR InterPro; IPR002219; -.
	DR InterPro; IPR002290; -.
	DR Pfam; PF00130; DAG_PEBind; 1.
	DR Pfam; PF00069; pkinase; 1.
	DR PRINTS; PR00068; DAGPDOMAIN.
	DR PROSITE; PS00479; DAG_PEBIND_DOM_1; 1.
	DR PROSITE; PS50081; DAG_PEBIND_DOM_2; 1.
	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
	DR PROSITE; PS00069; pkinase; 1.
	PRINTS; PR00068; DAGPDOMAIN.
	Pfam; PF00069; pkinase; 1.
	PRINTS; PR00068; DAGPDOMAIN.
	DR InterPro; IPR000719; -.
	DR InterPro; IPR002219; -.
	DR InterPro; IPR002290; -.
	DR Pfam; PF00130; DAG_PEBind; 1.
	DR Pfam; PF00069; pkinase; 1.
	DR PRINTS; PR00068; DAGPDOMAIN.
	DR PROSITE; PS00479; DAG_PEBIND_DOM_1; 1.
	DR PROSITE; PS50081; DAG_PEBIND_DOM_2; 1.
	DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
	DR PROSITE; PS00069; pkinase; 1.
	PRINTS; PR00068; DAGPDOMAIN.
	Pfam; PF00069; pkinase; 1.
	PRINTS; PR00068; DAGPDOMAIN.
	DR InterPro; IPR000719; -.
	DR InterPro; IPR002219; -.
	DR InterPro; IPR002290; -.
	DR Pfam; PF00130; DAG_PEBind; 1.
	DR Pfam; PF00069; pkinase; 1.
	DR PRINTS; PR00068; DAGPDOMAIN.
	DR PROSITE; PS00479; DAG_PEBIND_DOM_1; 1.
	DR PROSITE; PS50081; DAG_PEBIND_DOM_2; 1.
	DR PROSITE; PS00107; PROTEIN_KINASE_ATP

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
RW Transerase; Serine/threonine-protein kinase; Proto-oncogene; Zinc;
ATP-binding; Phorbol-ester binding.
FT DOMAIN 99 144 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 310 570 PROTEIN KINASE.
FT NP_BIND 316 324 ATP (BY SIMILARITY).
FT BINDING 336 336 ATP (BY SIMILARITY).
FT ACT_SITE 429 429 BY SIMILARITY.
FT SEQUENCE 606 AA; 67538 MW; 1A7EEB9A5D9DE152 CRC64;

Query Match 0.6%; Score 10; DB 1; Length 606;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 862 VKIGDFGLAT 871
Db 443 VKIGDFGLAT 452

Search completed: October 22, 2001, 01:31:53
Job time: 264 sec

